

Sequence listing

<110> Pieris Proteolab AG

<120> Soluble truncated polypeptides of the Nogo-A protein, methods for the production of such polypeptides and methods for identifying compounds having detectable affinity to a Nogo-A protein

<160> 18

<210> 1

<211> 1163

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat Nogo-A protein

<400> 1

Met	Glu	Asp	Ile	Asp	Gln	Ser	Ser	Leu	Val	Ser	Ser	Ser	Thr	Asp	1	5	10	15
Ser	Pro	Pro	Arg	Pro	Pro	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Thr	20	25	30	
Glu	Pro	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	35	40	45	
Glu	Asp	Asp	Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	50	55	60	
Pro	Ala	Ala	Gly	Leu	Ser	Ala	Ala	Ala	Val	Pro	Pro	Ala	Ala	Ala	65	70	75	
Ala	Pro	Leu	Leu	Asp	Phe	Ser	Ser	Asp	Ser	Val	Pro	Pro	Ala	Pro	80	85	90	
Arg	Gly	Pro	Leu	Pro	Ala	Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln	95	100	105	
Pro	Ser	Trp	Glu	Arg	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro	110	115	120	
Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu	125	130	135	
Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Gly	Ala	Ser	Pro	140	145	150	
Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro	Lys	155	160	165	
Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	Phe	Ala	Leu	Pro	170	175	180	
Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu	Lys	Ile	Met	185	190	195	
Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly	Gln	Glu				

200										205					210				
Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser					
				215					220					225					
Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu					
				230					235					240					
Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Glu					
				245					250					255					
Thr	Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Asn					
				260					265					270					
Pro	Phe	Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr					
				275					280					285					
Ser	Glu	Met	Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser					
				290					295					310					
Ala	Ile	Leu	Val	Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser					
				305					310					315					
Lys	Asp	Lys	Glu	Asp	Leu	Val	Cys	Ser	Ala	Ala	Leu	His	Ser	Pro					
				320					325					330					
Gln	Glu	Ser	Pro	Val	Gly	Lys	Glu	Asp	Arg	Val	Val	Ser	Pro	Glu					
				335					340					345					
Lys	Thr	Met	Asp	Ile	Phe	Asn	Glu	Met	Gln	Met	Ser	Val	Val	Ala					
				350					355					360					
Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp	Phe	Lys	Pro	Phe	Glu	Gln	Ala					
				365					370					375					
Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly	Ser	Arg	Asp	Val	Leu	Ala					
				380					385					390					
Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp	Arg	Lys	Cys	Leu	Glu					
				395					400					405					
Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys	Asp	Ser	Glu	Gly	Arg					
				410					415					420					
Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro	Glu	Pro	Val	Lys	Asp					
				425					430					435					
Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	Phe	Thr	Ser	Ala	Thr					
				440					445					450					
Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Leu	Glu	Asp	His	Thr					
				455					460					465					
Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	Arg	Lys	Ala					
				470					475					480					
Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys	Thr	Ser	Asn	Pro	Phe					
				485					490					495					
Leu	Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Tyr	Val	Thr	Thr	Asp					
				500					505					510					

Thr	Leu	Ser	Lys	Val	Thr	Glu	Ala	Ala	Val	Ser	Asn	Met	Pro	Glu	515	520	525
Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	530	535	540
Asn	Glu	Ala	Thr	Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp	545	550	555
Leu	Val	Gln	Thr	Ser	Glu	Ala	Ile	Gln	Glu	Ser	Leu	Tyr	Pro	Thr	560	565	570
Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser	575	580	585
Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu	590	595	600
Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	Val	Gln	Pro	Ser	Val	Ser	Pro	605	610	615
Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	Asp	Ser	Ile	Lys	Leu	Glu	620	625	630
Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met	Asn	Val	Ala	Leu	635	640	645
Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys	Glu	Pro	Glu	Ser	Phe	650	655	660
Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala	665	670	675
Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu	Pro	Ser	Pro	680	685	690
Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	Glu	Lys	Ser	Val	695	700	705
Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Glu	Ser	Glu	710	715	720
Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val	Pro	Gln	725	730	735
Thr	Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	Glu	Ser	Leu	Thr	Glu	740	745	750
Val	Ser	Glu	Thr	Val	Ala	Gln	His	Lys	Glu	Glu	Arg	Leu	Ser	Ala	755	760	765
Ser	Pro	Gln	Glu	Leu	Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Gln	Pro	770	775	780
Asn	Leu	His	Ser	Thr	Lys	Asp	Ala	Ala	Ser	Asn	Asp	Ile	Pro	Thr	785	790	795
Leu	Thr	Lys	Lys	Glu	Lys	Ile	Ser	Leu	Gln	Met	Glu	Glu	Phe	Asn	800	805	810

Thr	Ala	Ile	Tyr	Ser	Asn	Asp	Asp	Leu	Leu	Ser	Ser	Lys	Glu	Asp	
				815					820					825	
Lys	Ile	Lys	Glu	Ser	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	
				830					835					840	
Ile	Ile	Asp	Glu	Phe	Pro	Thr	Phe	Val	Ser	Ala	Lys	Asp	Asp	Ser	
				845					850					855	
Pro	Lys	Leu	Ala	Lys	Glu	Tyr	Thr	Asp	Leu	Glu	Val	Ser	Asp	Lys	
				860					865					870	
Ser	Glu	Ile	Ala	Asn	Ile	Gln	Ser	Gly	Ala	Asp	Ser	Leu	Pro	Cys	
				875					880					885	
Leu	Glu	Leu	Pro	Cys	Asp	Leu	Ser	Phe	Lys	Asn	Ile	Tyr	Pro	Lys	
				890					895					900	
Asp	Glu	Val	His	Val	Ser	Asp	Glu	Phe	Ser	Glu	Asn	Arg	Ser	Ser	
				905					910					915	
Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn	Val	Ser	Ala	Leu	Glu	
				920					925					930	
Pro	Gln	Thr	Glu	Met	Gly	Ser	Ile	Val	Lys	Ser	Lys	Ser	Leu	Thr	
				935					940					945	
Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	Lys	Glu	Asp	
				950					955					960	
Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser	
				965					970					975	
Val	Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	
				980					985					990	
Val	Phe	Gly	Ala	Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	
				995					1000					1005	
Ser	Ile	Val	Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	
				1010					1015					1020	
Val	Thr	Ile	Ser	Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	
				1030					1030					1035	
Gln	Lys	Ser	Asp	Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	
				1040					1045					1050	
Glu	Val	Ala	Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	
				1055					1060					1065	
Ala	Leu	Gly	His	Val	Asn	Ser	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	
				1070					1075					1080	
Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	
				1085					1090					1095	
Met	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr	
				1100					1105					1110	
Leu	Leu	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile	

	1115		1120		1125
Tyr Glu Arg His	Gln Val Gln Ile Asp	His Tyr Leu Gly Leu Ala			
	1130	1135		1140	
Asn Lys Ser Val	Lys Asp Ala Met Ala	Lys Ile Gln Ala Lys Ile			
	1145	1150		1155	
Pro Gly Leu Lys	Arg Lys Ala Asp				
	1160				

<210> 2
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> human Nogo-A protein

<400> 2

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	20	25 30
Pro Glu Asp Glu Glu	Glu Glu Glu Glu Glu	Glu Glu Glu Asp Glu
	35	40 45
Asp Glu Asp Leu Glu	Glu Leu Glu Val Leu	Glu Arg Lys Pro Ala
	50	55 60
Ala Gly Leu Ser Ala	Ala Pro Val Pro Thr	Ala Pro Ala Ala Gly
	65	70 75
Ala Pro Leu Met Asp	Phe Gly Asn Glu Phe	Val Pro Pro Ala Pro
	80	85 90
Arg Gly Pro Leu Pro	Ala Ala Pro Pro Val	Ala Pro Glu Arg Gln
	95	100 105
Pro Ser Trp Asp Pro	Ser Pro Val Ser Ser	Thr Val Pro Ala Pro
	110	115 120
Ser Pro Leu Ser Ala	Ala Ala Val Ser Pro	Ser Lys Leu Pro Glu
	125	130 135
Asp Asp Glu Pro Pro	Ala Arg Pro Pro Pro	Pro Pro Pro Ala Ser
	140	145 150
Val Ser Pro Gln Ala	Glu Pro Val Trp Thr	Pro Pro Ala Pro Ala
	155	160 165
Pro Ala Ala Pro Pro	Ser Thr Pro Ala Ala	Pro Lys Arg Arg Gly
	170	175 180
Ser Ser Gly Ser Val	Asp Glu Thr Leu Phe	Ala Leu Pro Ala Ala
	185	190 195

Ser	Glu	Pro	Val	Ile	Arg	Ser	Ser	Ala	Glu	Asn	Met	Glu	Leu	Lys	200	205	210
Glu	Gln	Pro	Gly	Asn	Thr	Ile	Ser	Ala	Gly	Gln	Glu	Asp	Phe	Pro	215	220	225
Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser	Leu	Ser	Pro	230	235	240
Leu	Ser	Ala	Ala	Ser	Phe	Lys	Glu	His	Glu	Tyr	Leu	Glu	Asn	Leu	245	250	255
Ser	Thr	Val	Leu	Pro	Thr	Glu	Gly	Thr	Leu	Gln	Glu	Asn	Val	Ser	260	265	270
Glu	Ala	Ser	Lys	Glu	Val	Ser	Glu	Lys	Ala	Lys	Thr	Leu	Leu	Ile	275	280	285
Asp	Arg	Asp	Leu	Thr	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	290	295	300
Gly	Ser	Ser	Phe	Ser	Val	Ser	Pro	Lys	Ala	Glu	Ser	Ala	Val	Ile	305	310	315
Val	Ala	Asn	Pro	Arg	Glu	Glu	Ile	Ile	Val	Lys	Asn	Lys	Asp	Glu	320	325	330
Glu	Glu	Lys	Leu	Val	Ser	Asn	Asn	Ile	Leu	His	Asn	Gln	Gln	Glu	335	340	345
Leu	Pro	Thr	Ala	Leu	Thr	Lys	Leu	Val	Lys	Glu	Asp	Glu	Val	Val	350	355	360
Ser	Ser	Glu	Lys	Ala	Lys	Asp	Ser	Phe	Asn	Glu	Lys	Arg	Val	Ala	365	370	385
Val	Glu	Ala	Pro	Met	Arg	Glu	Glu	Tyr	Ala	Asp	Phe	Lys	Pro	Phe	380	385	390
Glu	Arg	Val	Trp	Glu	Val	Lys	Asp	Ser	Lys	Glu	Asp	Ser	Asp	Met	395	400	405
Leu	Ala	Ala	Gly	Gly	Lys	Ile	Glu	Ser	Asn	Leu	Glu	Ser	Lys	Val	410	415	420
Asp	Lys	Lys	Cys	Phe	Ala	Asp	Ser	Leu	Glu	Gln	Thr	Asn	His	Glu	425	430	435
Lys	Asn	Ser	Glu	Ser	Ser	Asn	Asp	Asp	Thr	Ser	Phe	Pro	Ser	Thr	440	445	450
Pro	Glu	Gly	Ile	Lys	Asp	Arg	Pro	Gly	Ala	Tyr	Ile	Thr	Cys	Ala	455	460	465
Pro	Phe	Asn	Pro	Ala	Ala	Thr	Glu	Ser	Ile	Ala	Thr	Asn	Ile	Phe	470	475	480
Pro	Leu	Leu	Gly	Asp	Pro	Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	485	490	495
Lys	Ile	Glu	Glu	Lys	Lys	Ala	Gln	Ile	Val	Thr	Glu	Lys	Asn	Thr			

				500						505					510
Ser	Thr	Lys	Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala	Ala	Gln	Glu	Ser	
				515					520					525	
Glu	Thr	Asp	Tyr	Val	Thr	Thr	Asp	Asn	Leu	Thr	Lys	Val	Thr	Glu	
				530					535					540	
Glu	Val	Val	Ala	Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val	
				545					550					555	
Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr	Lys	
				560					565					570	
Ile	Ala	Tyr	Glu	Thr	Lys	Met	Asp	Leu	Val	Gln	Thr	Ser	Glu	Val	
				575					580					585	
Met	Gln	Glu	Ser	Leu	Tyr	Pro	Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe	
				590					595					600	
Glu	Glu	Ser	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	
				605					610					615	
Met	Glu	Ala	Pro	Leu	Asn	Ser	Ala	Val	Pro	Ser	Ala	Gly	Ala	Ser	
				620					625					630	
Val	Ile	Gln	Pro	Ser	Ser	Ser	Pro	Leu	Glu	Ala	Ser	Ser	Val	Gln	
				635					640					645	
Tyr	Glu	Ser	Ile	Lys	His	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	
				650					655					660	
Glu	Ala	Met	Ser	Val	Ser	Leu	Lys	Lys	Val	Ser	Gly	Ile	Lys	Glu	
				665					670					675	
Glu	Ile	Lys	Glu	Pro	Glu	Asn	Ile	Asn	Ala	Ala	Leu	Gln	Glu	Thr	
				680					685					690	
Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	
				695					700					705	
Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro	Glu	Phe	Ser	Asp	Tyr	Ser	Glu	
				710					715					720	
Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro	Asp	His	Ser	Glu	Leu	Val	
				725					730					735	
Glu	Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	
				740					745					750	
Asp	Ser	Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp	Glu	Thr	Val	Met	
				755					760					765	
Leu	Val	Lys	Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu	Ser	Met	Ile	
				770					775					780	
Glu	Tyr	Glu	Gln	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Pro	Pro	Glu	Gly	
				785					790					795	
Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Lys	Leu	Ser	Leu	Asp	Asn	Thr	
				800					805					810	

Lys Asp Thr Leu	Leu Pro Asp Glu Val	Ser Thr Leu Ser Lys	Lys
815		820	825
Glu Lys Ile Pro	Ile Gln Met Glu Glu	Leu Ser Thr Ala Val	Tyr
830		835	840
Ser Asn Asp Asp	Leu Phe Ile Ser Lys	Glu Ala Gln Ile Arg	Glu
845		850	855
Thr Glu Thr Phe	Ser Asp Ser Ser Pro	Ile Glu Ile Ile Asp	Glu
860		865	870
Phe Pro Thr Leu	Ile Ser Ser Lys Thr	Asp Ser Phe Ser Lys	Leu
875		880	885
Ala Arg Glu Tyr	Thr Asp Leu Glu Val	Ser His Lys Ser Glu	Ile
890		895	900
Ala Gln Ala Pro	Asp Gly Ala Gly Ser	Leu Pro Cys Thr Glu	Leu
905		910	915
Pro His Asp Leu	Ser Leu Lys Asn Ile	Gln Pro Lys Val Glu	Glu
920		925	930
Lys Ile Ser Phe	Ser Asp Asp Phe Ser	Lys Asn Gly Ser Ala	Thr
935		940	945
Ser Lys Val Leu	Leu Leu Pro Pro Asp	Val Ser Ala Leu Ala	Thr
950		955	960
Gln Ala Glu Ile	Glu Ser Ile Val Lys	Pro Lys Val Leu Val	Lys
965		970	975
Glu Ala Glu Lys	Lys Leu Pro Ser Asp	Thr Glu Lys Glu Asp	Arg
980		985	990
Ser Pro Ser Ala	Ile Phe Ser Ala Glu	Leu Ser Lys Thr Ser	Val
995		1000	1005
Val Asp Leu Leu	Tyr Trp Arg Asp Ile	Lys Lys Thr Gly Val	Val
1010		1015	1020
Phe Gly Ala Ser	Leu Phe Leu Leu Leu	Ser Leu Thr Val Phe	Ser
1025		1030	1035
Ile Val Ser Val	Thr Ala Tyr Ile Ala	Leu Ala Leu Leu Ser	Val
1040		1045	1050
Thr Ile Ser Phe	Arg Ile Tyr Lys Gly	Val Ile Gln Ala Ile	Gln
1055		1060	1065
Lys Ser Asp Glu	Gly His Pro Phe Arg	Ala Tyr Leu Glu Ser	Glu
1070		1075	1080
Val Ala Ile Ser	Glu Glu Leu Val Gln	Lys Tyr Ser Asn Ser	Ala
1085		1090	1095
Leu Gly His Val	Asn Cys Thr Ile Lys	Glu Leu Arg Arg Leu	Phe
1100		1105	1110

Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met
 1115 1120 1125
 Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu
 1130 1135 1140
 Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr
 1145 1150 1155
 Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn
 1160 1165 1170
 Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 1175 1180 1185
 Gly Leu Lys Arg Lys Ala Glu
 1190

<210> 3
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 <213> Artificial sequence

<220>
 <223> Primer

<400> 3

gctcagcggc cgagaccctt tttgctcttc ctg 33

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<220>
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<400> 4

gcttttaact atgctgccca tttctgt 27

<210> 5
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 <212> DNA
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<400> 5

ggtatccatg ttcttttaaaa gaggcctgcg ctacggtagc 40

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cacttcacag gtcaagctta ttaatggtga tggatgatggt gagcgctttt 50
 aactatgctg ccc 63

<210> 7
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ggtatccatg ttctttaaaa gaggcgccct gcgctacggt agc 43

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 <222> (34)
 <223> k: g or t

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gacattgagc tcacccagtc tccagcaatc atgkctgc 38

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 <212> DNA
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 <222> (37)...(39)
 <223> n: a, g, c or t; m: a or c

<220>
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<222> (43) ... (48)
 <223> n: a, g, c or t; m: a or c

<220>
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gcgcttcagc tcgagcttgg tcccagctcc gaacgtmna ggmnnmnnnta 50
acacattttg acagta 66
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<210> 10
 <211> 75
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (49) ... (54)
 <223> n: a, g, c or t; m: a or c

<220>
 <223> Primer

<400> 10

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gcgcttcagc tcgagcttgg tcccagctcc gaacgtaacc ggcacccgm 50
nmnnattttg acagtaatac gttgc 75
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<210> 11
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 <213> Mus musculus

<220>
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 <222> (1)...(121)
 <223> variable domain of the heavy chain of antibody IN-1

<400> 11

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Glu Val Lys Leu His Glu Ser Gly Pro Gly Leu Val Arg Pro Gly
1          5          10          15
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20        25        30
Asn Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu
35        40        45
Glu Trp Ile Gly Asp Ile Tyr Pro Gly Gly Gly Tyr Thr Asn Tyr
50        55        60
Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser
65        70        75
Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
80        85        90
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Ser Ala Val Tyr Phe Cys Ala Arg Phe Tyr Tyr Gly Ser Ser Tyr
 95 100 105

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 110 115 120

Ser

<210> 12

<211> 107

<212> PRT

<213> Artificial sequence

<220>

<221>

<222> (1)...(107)

<223> variable domain of the light chain of the antibody II.1.8

<400> 12

Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ala Ala Ser Val
 1 5 10 15

Gly Glu Thr Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr
 20 25 30

Gly Ala Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln
 35 40 45

Leu Leu Ile Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile
 65 70 75

Ser Ser Leu His Pro Asp Asp Val Ala Thr Tyr Tyr Cys Gln Asn
 80 85 90

Ile Asn Arg Val Pro Val Thr Phe Gly Ala Gly Thr Lys Leu Glu
 95 100 105

Ile Lys

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<222> (85)...(2238)

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                        -21 -20                        -15

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Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ser Phe
                        -10                        -5      -1    1

aaa gaa cat gga tac ctt ggt aac tta tca gca gtg tca tcc tca 135
Lys Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser
                        5                        10      15

gaa gga aca att gaa gaa act tta aat gaa gct tct aaa gag ttg 180
Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu
                        20                        25      30

cca gag agg gca aca aat cca ttt gta aat aga gat tta gca gaa 225
Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu
                        35                        40      45

ttt tca gaa tta gaa tat tca gaa atg gga tca tct ttt aaa ggc 270
Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly
                        50                        55      60

tcc cca aaa gga gag tca gcc ata tta gta gaa aac act aag gaa 315
Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu
                        65                        70      75

gaa gta att gtg agg agt aaa gac aaa gag gat tta gtt tgt agt 360
Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser
                        80                        85      90

gca gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa gac 405
Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp
                        95                        100     105

aga gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg 450
Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met
                        110                        115     120

cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt 495
Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe
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aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga 540
Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
140 145 150

agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg 585
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val
155 160 165

gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg 630
Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly
170 175 180

aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc 675
Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
185 190 195

cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct 720
Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala
200 205 210

tcc ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct 765
Ser Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro
215 220 225

ttg tta gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa 810
Leu Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
230 235 240

ata gaa gaa agg aag gcc caa att ata aca gag aag act agc ccc 855
Ile Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro
245 250 255

aaa acg tca aat cct ttc ctt gta gca gta cag gat tct gag gca 900
Lys Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala
260 265 270

gat tat gtt aca aca gat acc tta tca aag gtg act gag gca gca 945
Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala
275 280 285

gtg tca aac atg cct gaa ggt ctg acg cca gat tta gtt cag gaa 990
Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu
290 295 300

gca tgt gaa agt gaa ctg aat gaa gcc aca ggt aca aag att gct 1035
Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala
305 310 315

tat gaa aca aaa gtg gac ttg gtc caa aca tca gaa gct ata caa 1080
Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln
320 325 330

gaa tca ctt tac ccc aca gca cag ctt tgc cca tca ttt gag gaa 1125
Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu
335 340 345

gct gaa gca act ccg tca cca gtt ttg cct gat att gtt atg gaa 1170
Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
350 355 360

gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta gtg 1215

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Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	Val		
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cag	ccc	agt	gta	tcc	cca	ctg	gaa	gca	cct	cct	cca	gtt	agt	tat	1260	
Gln	Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr		
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gac	agt	ata	aag	ctt	gag	cct	gaa	aac	ccc	cca	cca	tat	gaa	gaa	1305	
Asp	Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu		
		395					400					405				
gcc	atg	aat	gta	gca	cta	aaa	gct	ttg	gga	aca	aag	gaa	gga	ata	1350	
Ala	Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile		
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Lys	Glu	Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala		
		425					430					435				
cct	tat	ata	tcc	att	gcg	tgt	gat	tta	att	aaa	gaa	aca	aag	ctc	1440	
Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu		
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Lys	Phe	Glu	Lys	Ser	Val	Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp		
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Ser	Ser	Pro	Glu	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser		
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att	cct	gaa	gtc	cca	caa	aca	caa	gag	gag	gct	gtg	atg	ctc	atg	1620	
Ile	Pro	Glu	Val	Pro	Gln	Thr	Gln	Glu	Glu	Ala	Val	Met	Leu	Met		
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Lys	Glu	Ser	Leu	Thr	Glu	Val	Ser	Glu	Thr	Val	Ala	Gln	His	Lys		
		515					520					525				
gag	gag	aga	ctt	agt	gcc	tca	cct	cag	gag	cta	gga	aag	cca	tat	1710	
Glu	Glu	Arg	Leu	Ser	Ala	Ser	Pro	Gln	Glu	Leu	Gly	Lys	Pro	Tyr		
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tta	gag	tct	ttt	cag	ccc	aat	tta	cat	agt	aca	aaa	gat	gct	gca	1755	
Leu	Glu	Ser	Phe	Gln	Pro	Asn	Leu	His	Ser	Thr	Lys	Asp	Ala	Ala		
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tct	aat	gac	att	cca	aca	ttg	acc	aaa	aag	gag	aaa	att	tct	ttg	1800	
Ser	Asn	Asp	Ile	Pro	Thr	Leu	Thr	Lys	Lys	Glu	Lys	Ile	Ser	Leu		
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caa	atg	gaa	gag	ttt	aat	act	gca	att	tat	tca	aat	gat	gac	tta	1845	
Gln	Met	Glu	Glu	Phe	Asn	Thr	Ala	Ile	Tyr	Ser	Asn	Asp	Asp	Leu		
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Leu	Ser	Ser	Lys	Glu	Asp	Lys	Ile	Lys	Glu	Ser	Glu	Thr	Phe	Ser		

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gat tca tct ccg att gag ata	ata gat gaa ttt ccc acg ttt gtc	1935	
Asp Ser Ser Pro Ile Glu Ile	Ile Asp Glu Phe Pro Thr Phe Val		
605	610	615	
agt gct aaa gat gat tct cct	aaa tta gcc aag gag tac act gat	1980	
Ser Ala Lys Asp Asp Ser Pro	Lys Leu Ala Lys Glu Tyr Thr Asp		
620	625	630	
cta gaa gta tcc gac aaa agt	gaa att gct aat atc caa agc ggg	2025	
Leu Glu Val Ser Asp Lys Ser	Glu Ile Ala Asn Ile Gln Ser Gly		
635	640	645	
gca gat tca ttg cct tgc tta	gaa ttg ccc tgt gac ctt tct ttc	2070	
Ala Asp Ser Leu Pro Cys Leu	Glu Leu Pro Cys Asp Leu Ser Phe		
650	655	660	
aag aat ata tat cct aaa gat	gaa gta cat gtt tca gat gaa ttc	2115	
Lys Asn Ile Tyr Pro Lys Asp	Glu Val His Val Ser Asp Glu Phe		
665	670	675	
tcc gaa aat agg tcc agt gta	tct aag gca tcc ata tcg cct tca	2160	
Ser Glu Asn Arg Ser Ser Val	Ser Lys Ala Ser Ile Ser Pro Ser		
680	685	690	
aat gtc tct gct ttg gaa cct	cag aca gaa atg ggc agc ata gtt	2205	
Asn Val Ser Ala Leu Glu Pro	Gln Thr Glu Met Gly Ser Ile Val		
695	700	705	
aaa agc gct tgg cgt cac ccg	cag ttc ggt ggt taa taa gctt	2248	
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                        -21 -20                        -15

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Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Glu Thr
                        -10                        -5      -1   1

ctt ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc tct 135
Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser
                        5                        10      15

gca gaa aaa att atg gat ttg atg gag cag cca ggt aac act gtt 180
Ala Glu Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val
                        20                        25      30

tcg tct ggt caa gag gat ttc cca tct gtc ctg ctt gaa act gct 225
Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala
                        35                        40      45

gcc tct ctt cct tct cta tct cct ctc tca act gtt tct ttt aaa 270
Ala Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys
                        50                        55      60

gaa cat gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa 315
Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu
                        65                        70      75

gga aca att gaa gaa act tta aat gaa gct tct aaa gag ttg cca 360
Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro
                        80                        85      90

gag agg gca aca aat cca ttt gta aat aga gat tta gca gaa ttt 405
Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe
                        95                        100     105

tca gaa tta gaa tat tca gaa atg gga tca tct ttt aaa ggc tcc 450
Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly Ser
                        110     115     120

cca aaa gga gag tca gcc ata tta gta gaa aac act aag gaa gaa 495
Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu
                        125     130     135

gta att gtg agg agt aaa gac aaa gag gat tta gtt tgt agt gca 540
Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala
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gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa gac aga 585
Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg
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gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg cag 630
Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln
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atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt aag 675

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Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys
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cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga agt 720
Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser
200                               205               210

agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac 765
Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
215                               220               225

aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag 810
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys
230                               235               240

gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca 855
Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro
245                               250               255

gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct tcc 900
Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser
260                               265               270

ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct ttg 945
Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu
275                               280               285

tta gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata 990
Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile
290                               295               300

gaa gaa agg aag gcc caa att ata aca gag aag act agc ccc aaa 1035
Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys
305                               310               315

acg tca aat cct ttc ctt gta gca gta cag gat tct gag gca gat 1080
Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp
320                               325               330

tat gtt aca aca gat acc tta tca aag gtg act gag gca gca gtg 1125
Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val
335                               340               345

tca aac atg cct gaa ggt ctg acg cca gat tta gtt cag gaa gca 1170
Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala
350                               355               360

tgt gaa agt gaa ctg aat gaa gcc aca ggt aca aag att gct tat 1215
Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr
365                               370               375

gaa aca aaa gtg gac ttg gtc caa aca tca gaa gct ata caa gaa 1260
Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln Glu
380                               385               390

tca ctt tac ccc aca gca cag ctt tgc cca tca ttt gag gaa gct 1305
Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala
395                               400               405

gaa gca act ccg tca cca gtt ttg cct gat att gtt atg gaa gca 1350
Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala

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Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	Val	Gln	
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ccc	agt	gta	tcc	cca	ctg	gaa	gca	cct	cct	cca	gtt	agt	tat	gac	1440
Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	Asp	
		440					445					450			
agt	ata	aag	ctt	gag	cct	gaa	aac	ccc	cca	cca	tat	gaa	gaa	gcc	1485
Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	
		455					460					465			
atg	aat	gta	gca	cta	aaa	gct	ttg	gga	aca	aag	gaa	gga	ata	aaa	1530
Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys	
		470					475					480			
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Glu	Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	
		485					490					495			
tat	ata	tcc	att	gcg	tgt	gat	tta	att	aaa	gaa	aca	aag	ctc	tcc	1620
Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	
		500					505					510			
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Thr	Glu	Pro	Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	
		515					520					525			
ttc	gag	aag	tcg	gtg	ccc	gaa	cac	gct	gag	cta	gtg	gag	gat	tcc	1710
Phe	Glu	Lys	Ser	Val	Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp	Ser	
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Ser	Pro	Glu	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	
		545					550					555			
cct	gaa	gtc	cca	caa	aca	caa	gag	gag	gct	gtg	atg	ctc	atg	aag	1800
Pro	Glu	Val	Pro	Gln	Thr	Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	
		560					565					570			
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Glu	Arg	Leu	Ser	Ala	Ser	Pro	Gln	Glu	Leu	Gly	Lys	Pro	Tyr	Leu	
		590					595					600			
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Glu	Ser	Phe	Gln	Pro	Asn	Leu	His	Ser	Thr	Lys	Asp	Ala	Ala	Ser	
		605					610					615			
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Asn	Asp	Ile	Pro	Thr	Leu	Thr	Lys	Lys	Glu	Lys	Ile	Ser	Leu	Gln	
		620					625					630			
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		635					640					645			

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tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt gtc agt 2115
Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser
      665                      670                      675

gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat cta 2160
Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu
      680                      685                      690

gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca 2205
Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
      695                      700                      705

gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag 2250
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys
      710                      715                      720

aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc 2295
Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser
      725                      730                      735

gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca aat 2340
Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn
      740                      745                      750

gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa 2385
Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys
      755                      760                      765

agc gct tgg cgt cac ccg cag ttc ggt ggt taa taa gctt          2425
Ser Ala Trp Arg His Pro Gln Phe Gly Gly End
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                        -21 -20                               -15

gca gtg gca ctg gct ggt ttc gct acc gta gcg cag gcc gct agc   90
Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ala Ser
                        -10                               -5                               -1

tgg agc cac ccg cag ttc gaa aaa ggc gcc tct ttt aaa gaa cat 135
Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Phe Lys Glu His
                        5                               10                               15

gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa gga aca 180
Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr
                        20                               25                               30

att gaa gaa act tta aat gaa gct tct aaa gag ttg cca gag agg 225
Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg
                        35                               40                               45

gca aca aat cca ttt gta aat aga gat tta gca gaa ttt tca gaa 270
Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu
                        50                               55                               60

tta gaa tat tca gaa atg gga tca tct ttt aaa ggc tcc cca aaa 315
Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys
                        65                               70                               75

gga gag tca gcc ata tta gta gaa aac act aag gaa gaa gta att 360
Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile
                        80                               85                               90

gtg agg agt aaa gac aaa gag gat tta gtt tgt agt gca gcc ctt 405
Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala Ala Leu
                        95                               100                              105

cac agt cca caa gaa tca cct gtg ggt aaa gaa gac aga gtt gtg 450
His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg Val Val
                        110                              115                              120

tct cca gaa aag aca atg gac att ttt aat gaa atg cag atg tca 495
Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln Met Ser
                        125                              130                              135

gta gta gca cct gtg agg gaa gag tat gca gac ttt aag cca ttt 540
Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe
                        140                              145                              150

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gaa caa gca tgg gaa gtg aaa gat act tat gag gga agt agg gat 585
Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp
155 160 165

gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac aga aaa 630
Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys
170 175 180

tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat agt 675
Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser
185 190 195

gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct 720
Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
200 205 210

gtg aag gac agc tcc aga gca tat att acc tgt gct tcc ttt acc 765
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr
215 220 225

tca gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa 810
Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu
230 235 240

gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa 855
Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu
245 250 255

agg aag gcc caa att ata aca gag aag act agc ccc aaa acg tca 900
Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser
260 265 270

aat cct ttc ctt gta gca gta cag gat tct gag gca gat tat gtt 945
Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val
275 280 285

aca aca gat acc tta tca aag gtg act gag gca gca gtg tca aac 990
Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn
290 295 300

atg cct gaa ggt ctg acg cca gat tta gtt cag gaa gca tgt gaa 1035
Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
305 310 315

agt gaa ctg aat gaa gcc aca ggt aca aag att gct tat gaa aca 1080
Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr
320 325 330

aaa gtg gac ttg gtc caa aca tca gaa gct ata caa gaa tca ctt 1125
Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu
335 340 345

tac ccc aca gca cag ctt tgc cca tca ttt gag gaa gct gaa gca 1170
Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala Glu Ala
350 355 360

act ccg tca cca gtt ttg cct gat att gtt atg gaa gca cca tta 1215
Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu
365 370 375

aat tct ctc ctt cca agc gct ggt gct tct gta gtg cag ccc agt 1260

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Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	Val	Gln	Pro	Ser			
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gta	tcc	cca	ctg	gaa	gca	cct	cct	cca	gtt	agt	tat	gac	agt	ata	1305		
Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	Asp	Ser	Ile			
		395					400					405					
aag	ctt	gag	cct	gaa	aac	ccc	cca	cca	tat	gaa	gaa	gcc	atg	aat	1350		
Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met	Asn			
		410					415					420					
gta	gca	cta	aaa	gct	ttg	gga	aca	aag	gaa	gga	ata	aaa	gag	cct	1395		
Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys	Glu	Pro			
		425					430					435					
gaa	agt	ttt	aat	gca	gct	gtt	cag	gaa	aca	gaa	gct	cct	tat	ata	1440		
Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile			
		440					445					450					
tcc	att	gcg	tgt	gat	tta	att	aaa	gaa	aca	aag	ctc	tcc	act	gag	1485		
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu			
		455					460					465					
cca	agt	cca	gat	ttc	tct	aat	tat	tca	gaa	ata	gca	aaa	ttc	gag	1530		
Pro	Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	Glu			
		470					475					480					
aag	tcg	gtg	ccc	gaa	cac	gct	gag	cta	gtg	gag	gat	tcc	tca	cct	1575		
Lys	Ser	Val	Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro			
		485					490					495					
gaa	tct	gaa	cca	gtt	gac	tta	ttt	agt	gat	gat	tcg	att	cct	gaa	1620		
Glu	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu			
		500					505					510					
gtc	cca	caa	aca	caa	gag	gag	gct	gtg	atg	ctc	atg	aag	gag	agt	1665		
Val	Pro	Gln	Thr	Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	Glu	Ser			
		515					520					525					
ctc	act	gaa	gtg	tct	gag	aca	gta	gcc	cag	cac	aaa	gag	gag	aga	1710		
Leu	Thr	Glu	Val	Ser	Glu	Thr	Val	Ala	Gln	His	Lys	Glu	Glu	Arg			
		530					535					540					
ctt	agt	gcc	tca	cct	cag	gag	cta	gga	aag	cca	tat	tta	gag	tct	1755		
Leu	Ser	Ala	Ser	Pro	Gln	Glu	Leu	Gly	Lys	Pro	Tyr	Leu	Glu	Ser			
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ttt	cag	ccc	aat	tta	cat	agt	aca	aaa	gat	gct	gca	tct	aat	gac	1800		
Phe	Gln	Pro	Asn	Leu	His	Ser	Thr	Lys	Asp	Ala	Ala	Ser	Asn	Asp			
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att	cca	aca	ttg	acc	aaa	aag	gag	aaa	att	tct	ttg	caa	atg	gaa	1845		
Ile	Pro	Thr	Leu	Thr	Lys	Lys	Glu	Lys	Ile	Ser	Leu	Gln	Met	Glu			
		575					580					585					
gag	ttt	aat	act	gca	att	tat	tca	aat	gat	gac	tta	ctt	tct	tct	1890		
Glu	Phe	Asn	Thr	Ala	Ile	Tyr	Ser	Asn	Asp	Asp	Leu	Leu	Ser	Ser			
		590					595					600					
aag	gaa	gac	aaa	ata	aaa	gaa	agt	gaa	aca	ttt	tca	gat	tca	tct	1935		
Lys	Glu	Asp	Lys	Ile	Lys	Glu	Ser	Glu	Thr	Phe	Ser	Asp	Ser	Ser			

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        605                610                615
ccg att gag ata ata gat gaa ttt ccc acg ttt gtc agt gct aaa 1980
Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser Ala Lys
        620                625                630

gat gat tct cct aaa tta gcc aag gag tac act gat cta gaa gta 2025
Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu Val
        635                640                645

tcc gac aaa agt gaa att gct aat atc caa agc ggg gca gat tca 2070
Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser
        650                655                660

ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat ata 2115
Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile
        665                670                675

tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat 2160
Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
        680                685                690

agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct 2205
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser
        695                700                705

gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa agc gct 2250
Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Ala
        710                715                720

cac cat cac cat cac cat taa taa gctt                2278
His His His His His His End
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<211> 798
<212> PRT
<213> Artificial sequence

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<221> SIGNAL
<222> (-21)...(-1)

<220>
<221> CHAIN
<222> (1)...(777)
<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

<220>
<221>
<222> (1)...(767)
<223> mature truncated Nogo-A

<220>
<221>
<222> (767)...(777)
<223> Strep-tag II affinity tag

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<400> 16

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								-21	-20						-15		
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			-10					-5				-1	1				
Leu	Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser			
		5					10					15					
Ala	Glu	Lys	Ile	Met	Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val			
		20					25					30					
Ser	Ser	Gly	Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala			
		35					40					45					
Ala	Ser	Leu	Pro	Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys			
		50					55					60					
Glu	His	Gly	Tyr	Leu	Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu			
		65					70					75					
Gly	Thr	Ile	Glu	Glu	Thr	Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro			
		80					85					90					
Glu	Arg	Ala	Thr	Asn	Pro	Phe	Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe			
		95					100					105					
Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	Gly	Ser	Ser	Phe	Lys	Gly	Ser			
		110					115					120					
Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val	Glu	Asn	Thr	Lys	Glu	Glu			
		125					130					135					
Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp	Leu	Val	Cys	Ser	Ala			
		140					145					150					
Ala	Leu	His	Ser	Pro	Gln	Glu	Ser	Pro	Val	Gly	Lys	Glu	Asp	Arg			
		155					160					165					
Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn	Glu	Met	Gln			
		170					175					180					
Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp	Phe	Lys			
		185					190					195					
Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly	Ser			
		200					205					210					
Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp			
		215					220					225					
Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys			
		230					235					240					
Asp	Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro			
		245					250					255					
Glu	Pro	Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser			

260							265				270			
Phe	Thr	Ser	Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu
		275					280					285		
Leu	Glu	Asp	His	Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile
		290					295					300		
Glu	Glu	Arg	Lys	Ala	Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys
		305					310					315		
Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp
		320					325					330		
Tyr	Val	Thr	Thr	Asp	Thr	Leu	Ser	Lys	Val	Thr	Glu	Ala	Ala	Val
		335					340					345		
Ser	Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu	Ala
		350					355					360		
Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr	Gly	Thr	Lys	Ile	Ala	Tyr
		365					370					375		
Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser	Glu	Ala	Ile	Gln	Glu
		380					385					390		
Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	Ala
		395					400					405		
Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu	Ala
		410					415					420		
Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	Val	Gln
		425					430					435		
Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	Asp
		440					445					450		
Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala
		455					460					465		
Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys
		470					475					480		
Glu	Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro
		485					490					495		
Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser
		500					505					510		
Thr	Glu	Pro	Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys
		515					520					525		
Phe	Glu	Lys	Ser	Val	Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp	Ser
		530					535					540		
Ser	Pro	Glu	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile
		545					550					555		
Pro	Glu	Val	Pro	Gln	Thr	Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys
		560					565					570		

Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys Glu
 575 580 585
 Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu
 590 595 600
 Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala Ser
 605 610 615
 Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln
 620 625 630
 Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu
 635 640 645
 Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp
 650 655 660
 Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser
 665 670 675
 Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu
 680 685 690
 Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
 695 700 705
 Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys
 710 715 720
 Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser
 725 730 735
 Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn
 740 745 750
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 Ser Ala Trp Arg His Pro Gln Phe Gly Gly
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<212> PRT

<213> Artificial sequence

<220>

<221> SIGNAL

<222> (-21)...(-1)

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<221> CHAIN

<222> (1)...(718)

<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

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<221>
 <222> (1)...(708)
 <223> mature truncated Nogo-A

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 <221>
 <222> (709)...(718)
 <223> Strep-tag affinity tag

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								-21	-20						-15		
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			-10					-5				-1	1				
Lys	Glu	His	Gly	Tyr	Leu	Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser			
		5					10					15					
Glu	Gly	Thr	Ile	Glu	Glu	Thr	Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu			
		20					25					30					
Pro	Glu	Arg	Ala	Thr	Asn	Pro	Phe	Val	Asn	Arg	Asp	Leu	Ala	Glu			
		35					40					45					
Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	Gly	Ser	Ser	Phe	Lys	Gly			
		50					55					60					
Ser	Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val	Glu	Asn	Thr	Lys	Glu			
		65					70					75					
Glu	Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp	Leu	Val	Cys	Ser			
		80					85					90					
Ala	Ala	Leu	His	Ser	Pro	Gln	Glu	Ser	Pro	Val	Gly	Lys	Glu	Asp			
		95					100					105					
Arg	Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn	Glu	Met			
		110					115					120					
Gln	Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp	Phe			
		125					130					135					
Lys	Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly			
		140					145					150					
Ser	Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val			
		155					160					165					
Asp	Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly			
		170					175					180					
Lys	Asp	Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr			
		185					190					195					
Pro	Glu	Pro	Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala			
		200					205					210					
Ser	Phe	Thr	Ser	Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro			
		215					220					225					

Leu	Leu	Glu	Asp	His	Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys
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Ile	Glu	Glu	Arg	Lys	Ala	Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro
		245					250					255		
Lys	Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala	Val	Gln	Asp	Ser	Glu	Ala
		260					265					270		
Asp	Tyr	Val	Thr	Thr	Asp	Thr	Leu	Ser	Lys	Val	Thr	Glu	Ala	Ala
		275					280					285		
Val	Ser	Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu
		290					295					300		
Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr	Gly	Thr	Lys	Ile	Ala
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Tyr	Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser	Glu	Ala	Ile	Gln
		320					325					330		
Glu	Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu
		335					340					345		
Ala	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu
		350					355					360		
Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	Val
		365					370					375		
Gln	Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr
		380					385					390		
Asp	Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu
		395					400					405		
Ala	Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile
		410					415					420		
Lys	Glu	Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala
		425					430					435		
Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu
		440					445					450		
Ser	Thr	Glu	Pro	Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala
		455					460					465		
Lys	Phe	Glu	Lys	Ser	Val	Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp
		470					475					480		
Ser	Ser	Pro	Glu	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser
		485					490					495		
Ile	Pro	Glu	Val	Pro	Gln	Thr	Gln	Glu	Glu	Ala	Val	Met	Leu	Met
		500					505					510		
Lys	Glu	Ser	Leu	Thr	Glu	Val	Ser	Glu	Thr	Val	Ala	Gln	His	Lys
		515					520					525		

Glu	Glu	Arg	Leu	Ser	Ala	Ser	Pro	Gln	Glu	Leu	Gly	Lys	Pro	Tyr	530	535	540
Leu	Glu	Ser	Phe	Gln	Pro	Asn	Leu	His	Ser	Thr	Lys	Asp	Ala	Ala	545	550	555
Ser	Asn	Asp	Ile	Pro	Thr	Leu	Thr	Lys	Lys	Glu	Lys	Ile	Ser	Leu	560	565	570
Gln	Met	Glu	Glu	Phe	Asn	Thr	Ala	Ile	Tyr	Ser	Asn	Asp	Asp	Leu	575	580	585
Leu	Ser	Ser	Lys	Glu	Asp	Lys	Ile	Lys	Glu	Ser	Glu	Thr	Phe	Ser	590	595	600
Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe	Pro	Thr	Phe	Val	605	610	615
Ser	Ala	Lys	Asp	Asp	Ser	Pro	Lys	Leu	Ala	Lys	Glu	Tyr	Thr	Asp	620	625	630
Leu	Glu	Val	Ser	Asp	Lys	Ser	Glu	Ile	Ala	Asn	Ile	Gln	Ser	Gly	635	640	645
Ala	Asp	Ser	Leu	Pro	Cys	Leu	Glu	Leu	Pro	Cys	Asp	Leu	Ser	Phe	650	655	660
Lys	Asn	Ile	Tyr	Pro	Lys	Asp	Glu	Val	His	Val	Ser	Asp	Glu	Phe	665	670	675
Ser	Glu	Asn	Arg	Ser	Ser	Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	680	685	690
Asn	Val	Ser	Ala	Leu	Glu	Pro	Gln	Thr	Glu	Met	Gly	Ser	Ile	Val	695	700	705
Lys	Ser	Ala	Trp	Arg	His	Pro	Gln	Phe	Gly	Gly					710	715	